

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/569,760
Source: IFWP
Date Processed by STIC: 03/13/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 03/13/2006

PATENT APPLICATION: US/10/569,760

TIME: 12:05:31

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\03132006\J569760.raw

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3 <110> APPLICANT: Janssen Pharmaceutica N.V.
5 <120> TITLE OF INVENTION: CHIMERIC GABAB RECEPTOR
7 <130> FILE REFERENCE: PRD 2108
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/569,760
C--> 9 <141> CURRENT FILING DATE: 2006-02-24
9 <150> PRIOR APPLICATION NUMBER: PCT/ EP03/10263
10 <151> PRIOR FILING DATE: 2003-09-13
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2886
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(2886)
24 <223> OTHER INFORMATION:
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29 Met Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
30 1 5 10 15
32 gcg ggc ggg gcg cag acc ccc aac gcc acc tca gaa ggt tgc cag atc 96
33 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
34 20 25 30
36 ata cac ccg ccc tgg gaa ggg ggc atc agg tac ccg ggc ctg act ccg 144
37 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
38 35 40 45
40 gac cag gtg aag gct atc aac ttc ctg cca gtg gac tat gag att gag 192
41 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
42 50 55 60
44 tat gtg tgc ccg ggg gag cgc gag gtg gtg ggg ccc aag gtc cgc aag 240
45 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
46 65 70 75 80
48 tgc ctg gcc aac ggc tcc tgg aca gat atg gac aca ccc agc cgc tgt 288
49 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
50 85 90 95
52 gtc cga atc tgc tcc aag tct tat ttg acc ctg gaa aat ggg aag gtt 336
53 Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
54 100 105 110
56 ttc ctg acg ggt ggg gac ctc cca gct ctg gac gga gcc ccg gtg gat 384
57 Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
58 115 120 125
60 ttc ccg tgt gac ccc gac ttc cat ctg gtg ggc agc tcc ccg agc atc 432

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61	Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	Arg	Ser	Ile	
62		130					135					140					
64	tgt	agt	cag	ggc	cag	tgg	agc	acc	ccc	aag	ccc	cac	tgc	cag	gtg	aat	480
65	Cys	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	Gln	Val	Asn	
66	145					150					155				160		
68	cga	acg	cca	cac	tca	gaa	cgg	cgc	gca	gtg	tac	atc	ggg	gca	ctg	ttt	528
69	Arg	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	Leu	Phe	
70				165						170				175			
72	ccc	atg	agc	ggg	ggc	tgg	cca	ggg	ggc	cag	gcc	tgc	cag	ccc	gcg	gtg	576
73	Pro	Met	Ser	Gly	Gly	Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	Pro	Ala	Val	
74			180					185					190				
76	gag	atg	gcg	ctg	gag	gac	gtg	aat	agc	cgc	agg	gac	atc	ctg	ccg	gac	624
77	Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp	
78		195					200					205					
80	tat	gag	ctc	aag	ctc	atc	cac	cac	gac	agc	aag	tgt	gat	cca	ggc	caa	672
81	Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln	
82	210					215					220						
84	gcc	acc	aag	tac	cta	tat	gag	ctg	ctc	tac	aac	gac	cct	atc	aag	atc	720
85	Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	Ile	Lys	Ile	
86	225				230					235			240				
88	atc	ctt	atg	cct	ggc	tgc	agc	tct	gtc	tcc	acg	ctg	gtg	gct	gag	gct	768
89	Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala	
90			245					250				255					
92	gct	agg	atg	tgg	aac	ctc	att	gtg	ctt	tcc	tat	gga	tcc	agc	tca	cca	816
93	Ala	Arg	Met	Trp	Asn	Leu	Ile	Val	Leu	Ser	Tyr	Gly	Ser	Ser	Ser	Pro	
94			260					265				270					
96	gcc	ctg	tca	aac	cgg	cag	cgt	ttc	ccc	act	ttc	ttc	cga	acg	cac	cca	864
97	Ala	Leu	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	
98		275					280					285					
100	tca	gcc	aca	ctc	cac	aac	cct	acc	cgc	gtg	aaa	ctc	ttt	gaa	aag	tgg	912
101	Ser	Ala	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	
102		290				295					300						
104	ggc	tgg	aag	aag	att	gct	acc	atc	cag	cag	acc	act	gag	gtc	ttc	act	960
105	Gly	Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	
106	305				310					315			320				
108	tcg	act	ctg	gac	gac	ctg	gag	gaa	cga	gtg	aag	gag	gct	gga	att	gag	1008
109	Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	
110			325					330				335					
112	att	act	ttc	cgc	cag	agt	ttc	ttc	tca	gat	cca	gct	gtg	ccc	gtc	aaa	1056
113	Ile	Thr	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	
114			340					345				350					
116	aac	ctg	aag	cgc	cag	gat	gcc	cga	atc	atc	gtg	gga	ctt	ttc	tat	gag	1104
117	Asn	Leu	Lys	Arg	Gln	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	
118		355					360					365					
120	act	gaa	gcc	cgg	aaa	gtt	ttt	tgt	gag	gtg	tac	aag	gag	cgt	ctc	ttt	1152
121	Thr	Glu	Ala	Arg	Lys	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe	
122		370				375				380							
124	ggg	aag	aag	tac	gtc	tgg	ttc	ctc	att	ggg	tgg	tat	gct	gac	aat	tgg	1200
125	Gly	Lys	Lys	Tyr	Val	Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	Asn	Trp	

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128	ttc aag atc tac gac cct tct atc aac tgc aca gtg gat gag atg act	1248						
129	Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr							
130			405		410		415	
132	gag gcg gtg gag ggc cac atc aca act gag att gtc atg ctg aat cct	1296						
133	Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro							
134			420		425		430	
136	gcc aat acc cgc agc att tcc aac atg aca tcc cag gaa ttt gtg gag	1344						
137	Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu							
138			435		440		445	
140	aaa cta acc aag cga ctg aaa aga cac cct gag gag aca gga ggc ttc	1392						
141	Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe							
142			450		455		460	
144	cag gag gca ccg ctg gcc tat gat gcc atc tgg gcc ttg gca ctg gcc	1440						
145	Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala							
146	465		470		475		480	
148	ctg aac aag aca tct gga gga ggc ggc cgt tct ggt gtg cgc ctg gag	1488						
149	Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu							
150			485		490		495	
152	gac ttc aac tac aac aac cag acc att acc gac caa atc tac cgg gca	1536						
153	Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala							
154			500		505		510	
156	atg aac tct tct tcc ttt gag ggt gtc tct ggc cat gtg gtg ttt gat	1584						
157	Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp							
158			515		520		525	
160	gcc agc ggc tct cgg atg gca tgg acg ctt atc gag cag ctt cag ggt	1632						
161	Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly							
162			530		535		540	
164	ggc agc tac aag aag att ggc tac tat gac agc acc aag gat gat ctt	1680						
165	Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu							
166	545		550		555		560	
168	tcc tgg tcc aaa aca gat aaa tgg att gga ggg tcc ccc cca gct gac	1728						
169	Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp							
170			565		570		575	
172	cag acc ctg gtc atc aag aca ttc cgc ttc ctg tca cag aaa ctc ttt	1776						
173	Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe							
174			580		585		590	
176	atc tcc gtc tca gtt ctc tcc agc ctg ggc att gtc cta gct gtt gtc	1824						
177	Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val							
178			595		600		605	
180	tgt ctg tcc ttt aac atc tac aac tca cat gtc cgt tat atc cag aac	1872						
181	Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn							
182			610		615		620	
184	tca cag ccc aac ctg aac aac ctg act gct gtg ggc tgc tca ctg gct	1920						
185	Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala							
186	625		630		635		640	
188	tta gct gct gtc ttc ccc ctg ggg ctc gat ggt tac cac att ggg agg	1968						
189	Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg							
190			645		650		655	

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194				660					665					670			
196	ggc	ttt	agt	ctg	ggc	tac	ggt	tcc	atg	ttc	acc	aag	att	tgg	tgg	gtc	2064
197	Gly	Phe	Ser	Leu	Gly	Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	Trp	Val	
198			675					680					685				
200	cac	acg	gtc	ttc	aca	aag	aag	gaa	gaa	aag	aag	gag	tgg	agg	aag	act	2112
201	His	Thr	Val	Phe	Thr	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	Lys	Thr	
202		690					695					700					
204	ctg	gaa	ccc	tgg	aag	ctg	tat	gcc	aca	gtg	ggc	ctg	ctg	gtg	ggc	atg	2160
205	Leu	Glu	Pro	Trp	Lys	Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val	Gly	Met	
206	705					710					715					720	
208	gat	gtc	ctc	act	ctc	gcc	atc	tgg	cag	atc	gtg	gac	cct	ctg	cac	cgg	2208
209	Asp	Val	Leu	Thr	Leu	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	His	Arg	
210				725					730					735			
212	acc	att	gag	aca	ttt	gcc	aag	gag	gaa	cct	aag	gaa	gat	att	gac	gtc	2256
213	Thr	Ile	Glu	Thr	Phe	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp	Val	
214				740					745					750			
216	tct	att	ctg	ccc	cag	ctg	gag	cat	tgc	agc	tcc	agg	aag	atg	aat	aca	2304
217	Ser	Ile	Leu	Pro	Gln	Leu	Glu	His	Cys	Ser	Ser	Arg	Lys	Met	Asn	Thr	
218			755					760					765				
220	tgg	ctt	ggc	att	ttc	tat	ggt	tac	aag	ggg	ctg	ctg	ctg	ctg	ctg	gga	2352
221	Trp	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	
222		770					775					780					
224	atc	ttc	ctt	gct	tat	gag	acc	aag	agt	gtg	tcc	act	gag	aag	atc	aat	2400
225	Ile	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn	
226	785					790					795					800	
228	gat	cac	cgg	gct	gtg	ggc	atg	gct	atc	tac	aat	gtg	gca	gtc	ctg	tgc	2448
229	Asp	His	Arg	Ala	Val	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu	Cys	
230				805					810					815			
232	ctc	atc	act	gct	cct	gtc	acc	atg	att	ctg	tcc	agc	cag	cag	gat	gca	2496
233	Leu	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	Asp	Ala	
234				820					825					830			
236	gcc	ttt	gcc	ttt	gcc	tct	ctt	gcc	ata	gtt	ttc	tcc	tcc	tat	atc	act	2544
237	Ala	Phe	Ala	Phe	Ala	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr	Ile	Thr	
238			835					840					845				
240	ctt	gtt	gtg	ctc	ttt	gtg	ccc	aag	atg	cgc	agg	ctg	atc	acc	cga	ggg	2592
241	Leu	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	Thr	Arg	Gly	
242		850					855					860					
244	gaa	tgg	cag	tcg	gag	gcg	cag	gac	acc	atg	aag	aca	ggg	tca	tcg	acc	2640
245	Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr	Met	Lys	Thr	Gly	Ser	Ser	Thr	
246	865					870					875					880	
248	aac	aac	aac	gag	gag	gag	aag	tcc	cgg	ctg	ttg	gag	aag	gag	aac	cgt	2688
249	Asn	Asn	Asn	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	Glu	Asn	Arg		
250				885					890					895			
252	gaa	ctg	gaa	aag	atc	att	gct	gag	aaa	gag	gag	cgt	gtc	tct	gaa	ctg	2736
253	Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	Ser	Glu	Leu	
254			900					905					910				
256	cgc	cat	caa	ctc	cag	tct	cgg	cag	cag	ctc	cgc	tcc	cgg	cgc	cac	cca	2784

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257 Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro
258          915          920          925
260 ccg aca ccc cca gaa ccc tct ggg ggc ctg ccc agg gga ccc cct gag      2832
261 Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu
262          930          935          940
264 ccc ccc gac cgg ctt agc tgt gat ggg agt cga gtg cat ttg ctt tat      2880
265 Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr
266 945          950          955          960
268 aag tga      2886
269 Lys
273 <210> SEQ ID NO: 2
274 <211> LENGTH: 961
275 <212> TYPE: PRT
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 2
280 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
281 1          5          10          15
284 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
285          20          25          30
288 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
289          35          40          45
292 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
293          50          55          60
296 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
297 65          70          75          80
300 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
301          85          90          95
304 Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
305          100         105         110
308 Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
309          115         120         125
312 Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile
313          130         135         140
316 Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn
317 145         150         155         160
320 Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe
321          165         170         175
324 Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val
325          180         185         190
328 Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp
329          195         200         205
332 Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln
333          210         215         220
336 Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile
337 225         230         235         240
340 Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
341          245         250         255
344 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro
345          260         265         270

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:24

L:535 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:532